CLAIM AMENDMENTS

1. (currently amended): A method to identify ~~a desired~~ region of [[a]] no more than 1,500 bases in an isolated a single copy of a target nucleic acid, said region to be targeted for ~~observation~~ interrogation, which method comprises

preparing a reaction mixture containing a sample containing said isolated target nucleic acid and isolated non-target nucleic acid with first and second identification probes that bracket said region,

which first identification probe comprises a first ~~oligomer~~ oligonucleotide specific for a sequence immediately upstream of said region coupled to a first particulate label, and

said second identification probe comprises a second ~~oligomer~~ oligonucleotide specific for a ~~proximal~~ sequence immediately downstream of said region coupled to a second particulate label;

wherein said first and second particulate labels are individually observable in a single copy of said nucleic acid molecule by microscopy,

displaying the reaction mixture on a surface under a microscope, and

observing the presence or absence of each member of any pairs of the first and second particulate labels as separate points in space, whereby the presence of said pairs identifies said desired region,

interrogating said region to genotype said single copy of said target nucleic acid.

2. (previously presented): The method of claim 1, wherein said first and second particulate labels comprise first and second fluorophores.

3. (previously presented): The method of claim 2, wherein said first and second fluorophores are distinguishable from each other.

4. (currently amended): The method of claim 1, wherein said first and second ~~oligomers~~ oligonucleotides are peptide nucleic acids.

5. (currently amended): The method of claim 1, wherein said target nucleic acid is single-stranded and said first and second ~~oligomers~~ oligonucleotides are complementary to the upstream and downstream sequences bracketing said region.

6. (currently amended): The method of claim 1, wherein said target nucleic acid is double-stranded and said first and second ~~oligomers~~ oligonucleotides form triplexes with said upstream and downstream sequences bracketing said region.

7. (currently amended): The method of claim 1, which is performed simultaneously on a multiplicity of target nucleic acids using a multiplicity of identification probes having particulate labels of differing hues coupled to ~~oligomers~~ oligonucleotides comprising sequences complementary to a multiplicity of said immediate upstream and downstream sequences bracketing a multiplicity of such regions.

8. (currently amended): A method to detect the presence of **[[**a**]]** an isolated single copy of a target nucleic acid of known sequence in a sample, which method comprises

preparing a reaction mixture containing **[[**a**]]** said sample to be tested for containing said isolated target nucleic acid and further containing isolated non-target nucleic acid and contacting said sample with at least first and second identification probes that bracket a region of no more than 1,500 bases of said target nucleic acid,

which first identification probe comprises a first ~~oligomer~~ oligonucleotide specific for a sequence immediately upstream of said region coupled to a first particulate label and said second identification probe comprises a second ~~oligomer~~ oligonucleotide specific for a ~~proximal~~ sequence immediately downstream of said region coupled to a second particulate label;

wherein said first and second particulate labels are individually observable by microscopy,

displaying the reaction mixture on a surface for microscope observation, and

observing the presence or absence of each member of any pairs of the first and second particulate labels as separate points in space, whereby the presence of said pairs indicates the presence of said target nucleic acid.

9. (previously presented): The method of claim 8, wherein said first and second particulate labels comprise first and second fluorophores.

10. (previously presented): The method of claim 9, wherein said first and second fluorophores are the same as each other.

11. (currently amended): The method of claim 8, wherein said first and second ~~oligomers.~~ oligonucleotides are peptide nucleic acids.

12. (currently amended): The method of claim 8, wherein said target nucleic acid is single-stranded and said first and second ~~oligomers.~~ oligonucleotides are complementary to the upstream and downstream sequences bracketing said region.

13. (currently amended): The method of claim 8, wherein said target nucleic acid is double-stranded and said first and second ~~oligomers.~~ oligonucleotides form triplexes with said upstream and downstream sequences bracketing said region.

14. (currently amended): The method of claim 8, which is performed simultaneously on a multiplicity of target nucleic acids, using a multiplicity of identification probes having particulate labels of differing hues for each known sequence targeted coupled to ~~oligomers.~~ oligonucleotides with different specificities according to the sequences targeted.

15. (currently amended): The method of claim 8, wherein said target nucleic acid of known sequence is ~~derived~~ isolated from an organism.

16. (original): The method of claim 15, wherein the organism is an infectious agent.

17. (original): The method of claim 15, wherein the organism is a human subject.

18-47. (canceled)